Spector . *1646*

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 08/902,576

CRF Processing Date: 11/23/98
Edited by: _____
Verified by: _____ (STIC staff)

☐ Changed a file from non-ASCII to ASCII

☑ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically:
_____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

ENTERED

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:
_____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
_____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:
_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:
_____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as_____ .

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:
_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:
_____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☐ Other:
_____
_____
_____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.   3/1/95

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/902,516*

DATE: 11/23/98
TIME: 12:08:42

INPUT SET: S29984.raw

𝓛. Spector

> This Raw Listing contains the General
> Information Section and those Sequences
> containing ERRORS.

*Does Not Comply
Corrected Diskette Needed*

```
 1                                    SEQUENCE LISTING
 2
 3   (1)     General Information:
 4
 5         (i) APPLICANT: Soo Hoo, William
 6
 7        (ii) TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
 8         COMPRISING GM-CSF ANDMETHODS OF MODULATING AN IMMUNE
 9         RESPONSE USING SAME
10
11       (iii) NUMBER OF SEQUENCES: 50
12
13       (iv) CORRESPONDENCE ADDRESS:
14             (A) ADDRESSEE: CAMPBELL & FLORES, LLP
15             (B) STREET: 4370 La Jolla Village Drive, Suite 700
16             (C) CITY: San Diego
17             (D) STATE: California
18             (E) COUNTRY: United States
19             (F) ZIP: 92121
20
21        (v) COMPUTER READABLE FORM:
22             (A) MEDIUM TYPE: Floppy disk
23             (B) COMPUTER: IBM PC compatible
24             (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25             (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
26
27       (vi) CURRENT APPLICATION DATA:
28             (A) APPLICATION NUMBER: US 08/902,516
29             (B) FILING DATE: 29-JUL-1997
30             (C) CLASSIFICATION:
31
32     (viii) ATTORNEY/AGENT INFORMATION:
33             (A) NAME: Campbell, Cathryn A.
34             (B) REGISTRATION NUMBER: 31,815
35             (C) REFERENCE/DOCKET NUMBER: P-IM 2442
36
37       (ix) TELECOMMUNICATION INFORMATION:
38             (A) TELEPHONE: (619)535-9001
39             (B) TELEFAX: (619)535-8949
40
41
```

ERRORED SEQUENCES FOLLOW:

```
42    (2) INFORMATION FOR SEQ ID NO:1:
43
44        (i) SEQUENCE CHARACTERISTICS:
45            (A) LENGTH: 660 base pairs
46            (B) TYPE: nucleic acid
47            (C) STRANDEDNESS: both
48            (D) TOPOLOGY: linear
49
50
51        (ix) FEATURE:
52            (A) NAME/KEY: CDS
53            (B) LOCATION: 1..660
54
55
56        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
57
58    ATG GAG ACA GAC ACA CTC CTG CTA TGG GTA CTG CTG CTC TGG GTT CCA
59    48
60    Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
61      1               5              10                  15
62
63    GGT TCC ACT GGG GAC TAT CCA TAT GAT GTT CCA GAT TAT GCT GGG GCC
64    96
65    Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ala
66                20              25                  30
67
68    CAA GCA CCC ACC CGC TCA CCC ATC ACT GTC ACC CGG CCT TGG AAG CAT
69    144
70    Gln Ala Pro Thr Arg Ser Pro Ile Thr Val Thr Arg Pro Trp Lys His
71                35              40                  45
72
73    GTA GAG GCC ATC AAA GAA GCC CTG AAC CTC CTG GAT GAC ATG CCT GTC
74    192
75    Val Glu Ala Ile Lys Glu Ala Leu Asn Leu Leu Asp Asp Met Pro Val
76          50              55                  60
77
78    ACG TTG AAT GAA GAG GTA GAA GTC GTC TCT AAC GAG TTC TCC TTC AAG
79    240
80    Thr Leu Asn Glu Glu Val Glu Val Val Ser Asn Glu Phe Ser Phe Lys
81      65              70                  75                  80
82
83    AAG CTA ACA TGT GTG CAG ACC CGC CTG AAG ATA TTC GAG CAG GGT CTA
84    288
85    Lys Leu Thr Cys Val Gln Thr Arg Leu Lys Ile Phe Glu Gln Gly Leu
86                85              90                  95
87
88    CGG GGC AAT TTC ACC AAA CTC AAG GGC GCC TTG AAC ATG ACA GCC AGC
89    336
90    Arg Gly Asn Phe Thr Lys Leu Lys Gly Ala Leu Asn Met Thr Ala Ser
91                100             105                 110
92
93    TAC TAC CAG ACA TAC TGC CCC CCA ACT CCG GAA ACG GAC TGT GAA ACA
94    384
```

INPUT SET: S29984.raw

```
 95    Tyr Tyr Gln Thr Tyr Cys Pro Pro Thr Pro Glu Thr Asp Cys Glu Thr
 96            115         120                 125
 97
 98    CAA GTT ACC ACC TAT GCG GAT TTC ATA GAC AGC CTT AAA ACC TTT CTG
 99    432
100    Gln Val Thr Thr Tyr Ala Asp Phe Ile Asp Ser Leu Lys Thr Phe Leu
101            130             135             140
102
103    ACT GAT ATC CCC TTT GAA TGC AAA AAA CCA GGC CAA AAA GTC GAC GAA
104    480
105    Thr Asp Ile Pro Phe Glu Cys Lys Lys Pro Gly Gln Lys Val Asp Glu
106    145             150                 155                 160
107
108    CAA AAA CTC ATC TCA GAA GAG GAT CTG AAT GCT GTG GGC CAG GAC ACG
109    528
110    Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ala Val Gly Gln Asp Thr
111                165             170                 175
112
113    CAG GAG GTC ATC GTG GTG CCA CAC TCC TTG CCC TTT AAG GTG GTG GTG
114    576
115    Gln Glu Val Ile Val Val Pro His Ser Leu Pro Phe Lys Val Val Val
116                180             185                 190
117
118    ATC TCA GCC ATC CTG GCC CTG GTG GTG CTC ACC ATC ATC TCC CTT ATC
119    624
120    Ile Ser Ala Ile Leu Ala Leu Val Val Leu Thr Ile Ile Ser Leu Ile
121            195             200                 205
122
123    ATC CTC ATC ATG CTT TGG CAG AAG AAG CCA CGT TAG                    660
124    Ile Leu Ile Met Leu Trp Gln Lys Lys Pro Arg
125            210             215                 220
126
127
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/902,516*

INPUT SET: S29984.raw

Line	Error	Original Text
45	Entered (660) and Calc. Seq. Length (36) differ	(A) LENGTH: 660 base pairs
123	# of Sequences for line conflicts w/ running total	ATC CTC ATC ATG CTT TGG CAG AAG AAG CCA CG